

188 nTyralaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208
1710 AACGTGAACACAGTGTCAAAATGAAGGAGGTGAACACATGTNTCAAACGCAAGATN 1769
208 InArgLThrGlnCysGlnMetLysGluAlaGluHisMetLysGlnAsnGlnAspA 228
1770 ATGTGAACAAACACACTGACAGCAGGAGTCTCTAGATCAGAAATATTTCACACAA 1829
228 snValasnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGln 248
1830 GCAAAATATGTGCTTCAACAGCAATAGTTCATGTCACATAAAGAACTGCAACAA 1889
248 exLysasnMetLysLeuGlnGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267
1890 AGCAAGATAACAATTCATNTTCATGAGGAGAAATGCN-CATCATCTCTCAAAA 1948
268 SerLysLysLeuThrLysLysLysLysLysLysLysLysLysLysLysLysLysLys 287
1949 GAGAAATATGAGGAGATATTTCATGAGGAGAAATGCN-CATCATCTCTCAAAA 2008
288 GluLysasnGluGluLysLysLysLysLysLysLysLysLysLysLysLysLysLys 307
2009 TCGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 2027
307 rGluLysGluLysAlaGlu 313

RESULT 29
US-09-604-287A-176
; Sequence 176, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-604-287A-176

Alignment Scores:
Pred. No.: 5.38e-124 Length: 317
Score: 1397.00 Matches: 288
Percent Similarity: 94.50% Conservative: 4
Best Local Similarity: 93.20% Mismatches: 13
Query Match: 41.05% Indels: 5
Gaps: 0
DB:
US-09-602-362E-15 (1-2030) x US-09-604-287A-176 (1-317)

US-09-602-362E-15 (1-2030) x US-09-604-287A-176 (1-317)
QY 1110 CAGGTTTCTCACACTCATGAAATGAAATATCTTACATGAAATGCAATGTGAAA 1169
Db 9 GluValSerHisThrHisGluasnGluasnTyLeuLeuHisGluasnCysMetLeuLys 28
QY 1170 AAGAAATGCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1229
Db 29 LysGluLysAlaMetLeuLysLeuGluLysLeuLysLeuLysLeuLysLeuLys 48
QY 1230 GAAATAAATGCTTGGAGCATTAGGATTTTAAAGAAAGAAAGAAAGAAAGAAAG 1289
Db 49 GluAsnLysTyLeuPheGluAspLysLysLysLysLysLysLysLysLysLys 68
QY 1290 ACCCTAAATGAAAGAGGAATCATTAACATAAGGGCATCTCAATATAGTGGGAGCTT 1349
Db 69 ThrLeuLysLeuLysGluLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 88

Alignment Scores:
Pred. No.: 5.38e-124 Length: 317
Score: 1397.00 Matches: 288
Percent Similarity: 94.50% Conservative: 4
Best Local Similarity: 93.20% Mismatches: 13
Query Match: 41.05% Indels: 5
Gaps: 0
DB:
US-09-602-362E-15 (1-2030) x US-09-285-480-176 (1-317)

QY 1410 GAAATAGAGAGAGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1469
Db 109 GluLysLeuLysGluLysGluLysGluLysGluLysGluLysGluLysGluLys 128
QY 1470 CATGATCAATGTCACATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1529
Db 129 HisAspGlnLeuValThrSerArgLysSerGlnGluProAlaPheHisLeuAlaGly 148
QY 1530 GCTGTTTCAAGAAAGAAATGATGTTGATGATGATGATGATGATGATGATGATG 1589
Db 149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyAsnAsnGlu 168
QY 1590 GCTCCATCAACCACTTTCTGAGCTCAAGAGAAATCCANAAGCTCAAGAAATTAATCT 1649
Db 168 IleuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysLysLeuLys 188
QY 1650 TTATGAGGAGATGCTCTAAGAGAGAAATACATTTGTTTCAGGAAACATGCAACAG 1709

US-09-602-362E-15 (1-2030) x US-09-285-480-176 (1-317)
QY 1110 CAGGTTTCTCACACTCATGAAATGAAATATCTTACATGAAATGCAATGTGAAA 1169
Db 9 GluValSerHisThrHisGluasnGluasnTyLeuLeuHisGluasnCysMetLeuLys 28
QY 1170 AAGAAATGCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1229
Db 29 LysGluLysAlaMetLeuLysLeuGluLysLeuLysLeuLysLeuLysLeuLys 48
QY 1230 GAAATAAATGCTTGGAGCATTAGGATTTTAAAGAAAGAAAGAAAGAAAGAAAG 1289
Db 49 GluAsnLysTyLeuPheGluAspLysLysLysLysLysLysLysLysLysLys 68
QY 1290 ACCCTAAATGAAAGAGGAATCATTAACATAAGGGCATCTCAATATAGTGGGAGCTT 1349
Db 69 ThrLeuLysLeuLysGluLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 88

US-09-602-362E-15 (1-2030) x US-09-285-480-176 (1-317)
QY 1110 CAGGTTTCTCACACTCATGAAATGAAATATCTTACATGAAATGCAATGTGAAA 1169
Db 9 GluValSerHisThrHisGluasnGluasnTyLeuLeuHisGluasnCysMetLeuLys 28
QY 1170 AAGAAATGCAATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1229
Db 29 LysGluLysAlaMetLeuLysLeuGluLysLeuLysLeuLysLeuLysLeuLys 48
QY 1230 GAAATAAATGCTTGGAGCATTAGGATTTTAAAGAAAGAAAGAAAGAAAGAAAG 1289
Db 49 GluAsnLysTyLeuPheGluAspLysLysLysLysLysLysLysLysLysLys 68
QY 1290 ACCCTAAATGAAAGAGGAATCATTAACATAAGGGCATCTCAATATAGTGGGAGCTT 1349
Db 69 ThrLeuLysLeuLysGluLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 88

				::				614
Db	GluGlnMetLysLysPheCysValLeuLysLysLeuSerGluAlaLysGluIle							
Qy	AAATCACAGTTAGAGAACCACCAAGCTTAAATGGCAACAAGAGCTCTCCAGTGTCAGATTG							3223
	LyseSerGlnLeuGluAanGlnLysValLysTrpGluGlnGluLeuCysSerVal----							632
Qy	CTTTTAANTCAAGAAGAAGAGACAGAGAAAATCTCGATATATTAAAGAAGAAAAATTAGA							3283
Db	-----							632
Qy	CCCGAAGAGCAACTTAGGAAAAAGTTAGAAAGTGAACACCAACTTGAAACAGACTCTCAGA							3343
Db	-----							632
Qy	ATACAGATATAGAATTGAAAAAGGTAAACAAGTAATTTGAATCAGGTTTCTCACACTCAT				:::			3403
Db	-----						-Arg-PheLeuThrIeuMe	638
Qy	GAAGTGAAATGATCTCTTTCATGAAAAATTGCATGT							3440
Db	tLysMetLysIleLeuSerTwrMetLysIleAlaCys							650

Db 41 SerAsnLysThrIleuGluLysGlyArgSerLysMetIleAlaCysProThrLys 60
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QY 1379 GAAACATCTACAAGAACGACGTACAAGTGTGGATGTGCAGTTCTCTAGAGCCCTATTTCAGT 1438
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Db 61 GluSerSerThrLysAlaSerAlaAsn----- 69
QY 1439 CTTTTTGCGCACCGACTATTCTCTAAGAGTGTGCACAGAAATTATACGTGTTTACCCTGATGCT 1498
Db 69 ----- 69
QY 1499 CTTCCTACCAAGATTATCTCTAAGAGTGTGCACAGAAATTATACGTGTTTACCCTGATGCT 1558
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QY 1559 ACATATCAAAGAATATCAAACATAAAATCAAAAAATAGAAGATCAGATGTTCCCATCA 1618
Db 70 -----AspGlnArgPheProSer 75
QY 1619 GAATCCAAACGACGAGAGATGAAGAATATTCTTGGGATTCCTGGGAGTCTCTTTGAGAGT 1678
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Db 76 GluSerLysGlnGluLeuAspGluGluIyrSerCysAspSerArgSerLeuPheGluSer 95
QY 1679 TCTGCCAAGACTCAAGTGTGTATACCTCGAGTCTATCTATCAAGAACTAATGAGATAAAT 1738
Db 96 SerAlaLysIleGlnValCysIleProGluSerIleIyrGlnLysValMetGluIleAsn 115
QY 1739 AGAAGAGTAGAAGAGCTTCTCGAAGACCATCTGCCTTCAAGCCCTGCCGTNGAATGCAA 1798
Db 116 ArgGluValGluGluProProLysLysProSerAlaPheLysProAlaIleGluMetGln 135
QY 1799 AAGACTGTTCCAAATAAAGCCTTTGAATTGAAGATGAACAACAATTTGAGAGAGCTCAG 1858
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Db 136 AsnSerValProAsnLysAlaPheGluLeuLysAsnGluGlnThrLeuArgAlaAspPro 155
QY 1859 ATGTTCCCCATCAGAATCCAAAACAAAGGACGATGAAGAAAATCTCTGGATTTCTGAGACT 1918
Db 156 MetPheProGluSerLysGlnLysAspTyrGluGluAsnSerTrpAspSerGluSer 175
QY 1919 CCCTGTGAGACGGTTTCACAGAGAGATGTGTATTTACCCAAGCTACACATCAAAAGAA 1978
Db 176 LeuCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGlu 195
QY 1979 TTCGATACCTTAAGTCGAAAAATTAGAAGAGTCTCTGTTTAAAGATGTCTCTCGAAGCCT 2038
Db 196 IleAspLysIleAsnGlnLysLeuGluSerProAsnLysAspGlyLeuLeuLysAla 215
QY 2039 ACTGTGGAAGGAAAGTTTCTCTCCAATAAAGCCTTAGAATTAAGACACAGAGAAACA 2098
Db 216 ThrCysGlyMetLysValSerIleProThrLysAlaLeuGluLeuLysAspMetGlnThr 235
QY 2099 TTCAAAGCAGAGTCTCTCGATAAAGATGGTCTCTTGAAGCCCTACCTGTGGGAAGAAAGTT 2158
Db 236 PheLysAlaGluProProGlyLysProSerAlaPheGluProAlaThrGluMetGlnLys 255
QY 2159 TCTCTTCCAAATAAAGCCTTAGAATTAAGAGACACAGAAACACTCAAAGCAGAGTCTCCT 2218
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Db 256 SerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAsp----- 273
QY 2219 GATAATGATGGTCTTCTGAAGCCTACCTGTGGAAGGAAAGTTTCTCTTCCAAATAAAGCT 2278
Db 273 ----- 273
QY 2279 TTAGAATTGAAGGACAGAGAAACATTCAAAGCAGCTCAGATGTTCCCATCAGAAATCCAAA 2338
Db 274 -----GluIleLeuProSerGluSerLys 281
QY 2339 CAAAAGGATGATGAAGAAAATTTCTGGGATTTTGAGAGTTTCTCTTGAGACTCTCTTTACAG 2398
Db 282 GlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThrValSerGln 301
QY 2399 AATGATGTGTGTTTACCAGGCTACATCAAAAAAGAAATTCGATACCTTAAGTGGGAAA 2458
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3284 CCCGAAGAGCAACTTAGGAAAAAGTTAGAGTGAACACCAACTTGAAACAGACTCTCAGA 3343
        632 ----- 632
3344 ATACAAGATATAGAAATTGAAAGCTGTAAACAAGTAATTGAACTCAGGTTTCTCACACTCAT 3403
        633 -----Arg-PheLeuThrLeuMe 638
3404 GAAAGTGAAGATGCATCTCTTTTCATGATAAATTGCATGT 3440
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638 tlybMetLysIleIleSerTyMetLysIleAlaCys 650

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US-09-604-287A-469
; Sequence 469, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (310)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: unsure
; LOCATION: (429)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: unsure
; LOCATION: (522)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-604-287A-469

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Alignment Scores:	2.24e-134	Length:	650
Pred. No.:	1769.50	Matches:	396
Score:	54.38%	Conservative:	112
Percent Similarity:	47.54%	Mismatches:	172
Best Local Similarity:	7.44%	Indels:	268
Query Match:	4	Gaps:	9
DB:			
		US-09-602-362E-26 (1-3673) x US-09-604-287A-469 (1-550)	

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	1 MetSerProAlaIysGluThrSerGluLysPheThrTrpAlaAlaLysGlyArgProArg	20
1259	AAGATCACATGGAGGAGAAAGAAACATCTGAAAGACTGAATGGCTGCAGGAGTAAACA	1318
	21 LysIleAlaTrpGluLysGluThrProValLysThrGlyCysValAlaArgValThr	40
1319	CCTAATPAAACATGAAGTTTTCGAAAAAGGAACATCTAATATGATTGCATCTCTCAACAAA	1378
	41 SerAsnLysThrLysValIleGluLysGlyArgSerLysMetIleAlaCysProThrLys	60
1379	GAAACATCTACAAAGCAAGTACAAATGTGGATGTGATGTTCTGTAGAGCCATATATCAAGT	1438
	61 GluSerSerThrLysAlaSerAlaSer-----	69